



Sequence Listing

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<120> NOVEL POLYPEPTIDES, THEIR NUCLEIC ACIDS, AND METHODS
FOR THEIR USE IN ANGIOGENESIS AND VASCULARIZATION

<130> P1776R2US

<141> 2000-10-05

<150> US 60/158,587

<151> 1999-10-07

<150> US 60/162,611

<151> 1999-10-28

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1 5

gcc ggc aag gtg ctg ctg gac gac acg gtg ccg ctg aca 128
Ala Gly Lys Val Leu Leu Asp Asp Thr Val Pro Leu Thr
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gca gcc atc gag gcg agc cag agc ctg cag tcc cac acg 167
Ala Ala Ile Glu Ala Ser Gln Ser Leu Gln Ser His Thr
25 30

gaa tat att att cga gtg caa aga gga att tct gtg gaa 206
Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser Val Glu
35 40 45

aac agc tgg cag att gtt aga aga tac agt gac ttt gat 245
Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp
50 55 60

ttg ctt aac aac agc tta cag att gca ggc cta agt cta 284
Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu
65 70

cct ctt cct ccc aaa aaa ttg att ggt aac atg gat cgt 323
Pro Leu Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg
75 80 85

gaa ttc ata gct gaa agg cag aaa ggt ctt cag aac tat 362
Glu Phe Ile Ala Glu Arg Gln Lys Gly Leu Gln Asn Tyr
90 95

ctc aac gtg atc aca aca aat cat atc ttg tct aat tgt 401
 Leu Asn Val Ile Thr Thr Asn His Ile Leu Ser Asn Cys
 100 105 110

gag ctg gtt aag aag ttt tta gat cca aac aac tat tcc 440
 Glu Leu Val Lys Lys Phe Leu Asp Pro Asn Asn Tyr Ser
 115 120 125

gca aac tat act gag att gcc ttg caa cag gtt tcc atg 479
 Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln Val Ser Met
 130 135

ttc ttc cga tca gaa cca aag tgg gag gtg gtg gaa cct 518
 Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu Pro
 140 145 150

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 Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe
 155 160

ttg atg aag att aaa aat cag cca aag gaa cgg cta gtg 596
 Leu Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val
 165 170 175

tta agc tgg gct gac ctt ggc cca gac aag tat ttg tca 635
 Leu Ser Trp Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser
 180 185 190

gat aaa gat ttt cag tgt cta atc aaa ctt ctg cct tct 674
 Asp Lys Asp Phe Gln Cys Leu Ile Lys Leu Leu Pro Ser
 195 200

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 Cys Leu His Pro Tyr Ile Tyr Arg Val Thr Phe Ala Thr
 205 210 215

gct aat gaa tcc tca gcg ttg cta att agg atg ttt aac 752
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 220 225

gaa aag gga aca ttg aag gat ctg atc tac aag gca aaa 791
 Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys Ala Lys
 230 235 240

cca aaa gac cca ttt cta aag aag tac tgc aac cct aag 830
 Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys
 245 250 255

aag att cag ggc ctg gaa ctc cag caa ata aaa aca tat 869
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 260 265

gga cgg caa ata tta gag gta ctg aag ttt ctt cat gac 908
 Gly Arg Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp
 270 275 280

aag gga ttc cct tat ggg cat ctt cac gcc tcc aat gtg 947
 Lys Gly Phe Pro Tyr Gly His Leu His Ala Ser Asn Val
 285 290

atg ctc gat ggg gac act tgt cgg ctg ctg gac ctt gag 986
Met Leu Asp Gly Asp Thr Cys Arg Leu Leu Asp Leu Glu
295 300 305

aat tcc tta ttg ggc ctg cct tcc ttc tac cga tct tat 1025
Asn Ser Leu Leu Gly Leu Pro Ser Phe Tyr Arg Ser Tyr
310 315 320

ttt tca caa ttc agg aaa atc aat aca ttg gaa agt gtg 1064
Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu Glu Ser Val
325 330

gat gtc cac tgc ttt ggc cac tta ctg tat gaa atg act 1103
Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met Thr
335 340 345

tat gga cga ccg cca gac tcg gtg cct gtg gac tcc ttc 1142
Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe
350 355

cct cct gcc ccg tcc atg gct gtg gtg gcc gtg ttg gag 1181
Pro Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu
360 365 370

tct acg ctg tct tgt gaa gcc tgt aaa aat ggc atg cct 1220
Ser Thr Leu Ser Cys Glu Ala Cys Lys Asn Gly Met Pro
375 380 385

acc atc tcc cgg ctc tta cag atg cca tta ttc agc gat 1259
Thr Ile Ser Arg Leu Leu Gln Met Pro Leu Phe Ser Asp
390 395

gtt tta cta acc act tct gaa aaa cca cag ttt aag atc 1298
Val Leu Leu Thr Thr Ser Glu Lys Pro Gln Phe Lys Ile
400 405 410

cct aca aag tta aaa gag gca ttg aga att gcc aaa gaa 1337
Pro Thr Lys Leu Lys Glu Ala Leu Arg Ile Ala Lys Glu
415 420

tgt ata gag aag aga cta att gag gaa cag aaa cag att 1376
Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Lys Gln Ile
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cac cag cat cga aga ctg aca aga gct cag tcc cac cat 1415
His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His
440 445 450

gga tct gag gag gaa aga aaa aaa aga aag att tta gct 1454
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cga aag aag tca aaa cga tct gct ctt gaa aat agt gaa 1493
Arg Lys Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu
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gag cat tca gcg agg tac agc aac tcc aat aat tca gga 1532
Glu His Ser Ala Arg Tyr Ser Asn Ser Asn Asn Ser Gly
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tct ggg gcc agc tca cct ctc acg tcc ccg tca tcg cca 1571

Ser Gly Ala Ser Ser Pro Leu Thr Ser Pro Ser Ser Pro
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 act cca ccc tct aca tca ggg ata tct gca tta cct cca 1610
 Thr Pro Pro Ser Thr Ser Gly Ile Ser Ala Leu Pro Pro
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 Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser
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 Thr Cys Asp His Ser Ala Pro Lys Ile Gly
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Gln	Ser	His	Thr	Glu	Tyr	Ile	Ile	Arg	Val	Gln	Arg	Gly	Ile	Ser
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Val	Glu	Asn	Ser	Trp	Gln	Ile	Val	Arg	Arg	Tyr	Ser	Asp	Phe	Asp
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Leu	Leu	Asn	Asn	Ser	Leu	Gln	Ile	Ala	Gly	Leu	Ser	Leu	Pro	Leu
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Pro	Pro	Lys	Lys	Leu	Ile	Gly	Asn	Met	Asp	Arg	Glu	Phe	Ile	Ala
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Glu	Arg	Gln	Lys	Gly	Leu	Gln	Asn	Tyr	Leu	Asn	Val	Ile	Thr	Thr
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Asn	His	Ile	Leu	Ser	Asn	Cys	Glu	Leu	Val	Lys	Lys	Phe	Leu	Asp
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Pro	Asn	Asn	Tyr	Ser	Ala	Asn	Tyr	Thr	Glu	Ile	Ala	Leu	Gln	Gln
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Pro	Leu	Lys	Asp	Ile	Gly	Trp	Arg	Ile	Arg	Lys	Lys	Tyr	Phe	Leu
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Ala	Asp	Leu	Gly	Pro	Asp	Lys	Tyr	Leu	Ser	Asp	Lys	Asp	Phe	Gln
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Cys	Leu	Ile	Lys	Leu	Leu	Pro	Ser	Cys	Leu	His	Pro	Tyr	Ile	Tyr
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 Ala Lys Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys
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 Lys Ile Gln Gly Leu Glu Leu Gln Gln Ile Lys Thr Tyr Gly Arg
 260 265 270
 Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp Lys Gly Phe Pro
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 Tyr Gly His Leu His Ala Ser Asn Val Met Leu Asp Gly Asp Thr
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 Cys Arg Leu Leu Asp Leu Glu Asn Ser Leu Leu Gly Leu Pro Ser
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 Phe Tyr Arg Ser Tyr Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu
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 Glu Ser Val Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met
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 Thr Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe Pro
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 Ser Cys Glu Ala Cys Lys Asn Gly Met Pro Thr Ile Ser Arg Leu
 380 385 390
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 Lys Pro Gln Phe Lys Ile Pro Thr Lys Leu Lys Glu Ala Leu Arg
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 Ile Ala Lys Glu Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Lys
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 Gln Ile His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His
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 Gly Ser Glu Glu Glu Arg Lys Lys Arg Lys Ile Leu Ala Arg Lys
 455 460 465
 Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu Glu His Ser Ala
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 Arg Tyr Ser Asn Ser Asn Asn Ser Gly Ser Gly Ala Ser Ser Pro
 485 490 495
 Leu Thr Ser Pro Ser Ser Pro Thr Pro Pro Ser Thr Ser Gly Ile
 500 505 510
 Ser Ala Leu Pro Pro Pro Pro Pro Pro Pro Pro Ala Ala
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 Pro Leu Pro Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Ser

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Trp Leu Asn Phe Ser Thr Pro Gln Ser Ala Lys Ser Pro		
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act gcc acc ttc gaa aaa cac gga gag cac cta ccc aga 569		
Thr Ala Thr Phe Glu Lys His Gly Glu His Leu Pro Arg		
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Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg Thr		
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Ile Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu		

75

80

85

gaa tca cag gga acc cat ctg gtt ggc ata gct ctt ccc 764
 Glu Ser Gln Gly Thr His Leu Val Gly Ile Ala Leu Pro
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cga ggt cat gat ggc atg agc caa cgt agt gta ggt ggc 803
 Arg Gly His Asp Gly Met Ser Gln Arg Ser Val Gly Gly
 105 110

aca ggg aac cat cgc cat tgg aat ggc agc ttc cac tcc 842
 Thr Gly Asn His Arg His Trp Asn Gly Ser Phe His Ser
 115 120 125

cgg aaa ggg tgt gct ttt cag gaa aag cca cct atg gag 881
 Arg Lys Gly Cys Ala Phe Gln Glu Lys Pro Pro Met Glu
 130 135

att agg gaa gaa aag aaa gaa gac aag gtg gaa aag ttg 920
 Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu Lys Leu
 140 145 150

cag ttt gaa gag gag gac ttt cct tcc ttg aat cca gaa 959
 Gln Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu
 155 160 165

gct ggc aaa cag cat cag cca tgc aga cct att ggg aca 998
 Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr
 170 175

cct tct gga gta tgg gaa aac ccg cct agt gcc aag caa 1037
 Pro Ser Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln
 180 185 190

ccc tcc aag atg cta gtt atc aaa aaa gtt tcc aaa gag 1076
 Pro Ser Lys Met Leu Val Ile Lys Lys Val Ser Lys Glu
 195 200

gat cct gct gct gcc ttc tct gct gca ttc acc tca cca 1115
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 205 210 215

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 220 225 230

gtt cca agt gtc tat aag aac ctg gtt cct aag cct gta 1193
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 235 240

cca cct cct tcc aag cct aat gca tgg aaa gct aac agg 1232
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 245 250 255

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 260 265

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 270 275 280

gta ctg gct agt ggt gca gct ctg agt tct ccc aaa gag 1349
 Val Leu Ala Ser Gly Ala Ala Leu Ser Ser Pro Lys Glu
 285 290 295

 agt ccc tcc agc acc acc cct cca att gag atc agc tcc 1388
 Ser Pro Ser Ser Thr Thr Pro Pro Ile Glu Ile Ser Ser
 300 305

 tct cgt ctg acc aag ttg acc cgc cga acc acc gac agg 1427
 Ser Arg Leu Thr Lys Leu Thr Arg Arg Thr Thr Asp Arg
 310 315 320

 aag agt gag ttc ctg aaa act ctg aag gat gac cgg aat 1466
 Lys Ser Glu Phe Leu Lys Thr Leu Lys Asp Asp Arg Asn
 325 330

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 Gly Asp Phe Ser Glu Asn Arg Asp Cys Asp Lys Leu Glu
 335 340 345

 gat ttg gag gac aac agc aca cct gaa cca aag gaa aat 1544
 Asp Leu Glu Asp Asn Ser Thr Pro Glu Pro Lys Glu Asn
 350 355 360

 ggg gag gaa ggc tgt cat caa aat ggt ctt gcc ctc cct 1583
 Gly Glu Gly Cys His Gln Asn Gly Leu Ala Leu Pro
 365 370

 gta gtg gaa gaa ggg gag gtt ctc tca cac tct cta gaa 1622
 Val Val Glu Glu Gly Glu Val Leu Ser His Ser Leu Glu
 375 380 385

 gca gag cac agg tta ttg aaa gct atg ggt tgg cag gaa 1661
 Ala Glu His Arg Leu Leu Lys Ala Met Gly Trp Gln Glu
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 tat cct gaa aat gat gag aat tgc ctt ccc ctc aca gag 1700
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 gat gag ctc aaa gag ttc cac atg aag aca gag cag ctg 1739
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 415 420 425

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 cgc agt tcc agt ctg ttc cct tgg aga agc act tgc 1817
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 440 445 450

 aaa gca gag ttt gag gac tca gac acc gaa acc agt agc 1856
 Lys Ala Glu Phe Glu Asp Ser Asp Thr Glu Thr Ser Ser
 455 460

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 Ser Glu Thr Ser Asp Asp Asp Ala Trp Lys
 465 470 474

catataaatg ctcacagtta aatctgaccc agtaaactct gtgtgttag 1940
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 35 40 45

Arg His Asn Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg
 50 55 60

Thr Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met Ile
 65 70 75

Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu Glu Ser Gln
 80 85 90

Gly Thr His Leu Val Gly Ile Ala Leu Pro Arg Gly His Asp Gly
 95 100 105

Met Ser Gln Arg Ser Val Gly Gly Thr Gly Asn His Arg His Trp
 110 115 120

Asn Gly Ser Phe His Ser Arg Lys Gly Cys Ala Phe Gln Glu Lys
 125 130 135

Pro Pro Met Glu Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu
 140 145 150

Lys Leu Gln Phe Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu
 155 160 165

Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr Pro Ser
 170 175 180

Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln Pro Ser Lys Met
 185 190 195

Leu Val Ile Lys Lys Val Ser Lys Glu Asp Pro Ala Ala Ala Phe
 200 205 210

Ser Ala Ala Phe Thr Ser Pro Gly Ser His His Ala Asn Gly Asn
 215 220 225

Lys	Leu	Ser	Ser	Val	Val	Pro	Ser	Val	Tyr	Lys	Asn	Leu	Val	Pro
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Lys	Pro	Val	Pro	Pro	Pro	Ser	Lys	Pro	Asn	Ala	Trp	Lys	Ala	Asn
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Arg	Met	Glu	His	Lys	Ser	Gly	Ser	Leu	Ser	Ser	Ser	Arg	Glu	Ser
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Ala	Phe	Thr	Ser	Pro	Ile	Ser	Val	Thr	Lys	Pro	Val	Val	Leu	Ala
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Ser	Gly	Ala	Ala	Leu	Ser	Ser	Pro	Lys	Glu	Ser	Pro	Ser	Ser	Thr
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Thr	Pro	Pro	Ile	Glu	Ile	Ser	Ser	Ser	Arg	Leu	Thr	Lys	Leu	Thr
				305					310				315	
Arg	Arg	Thr	Thr	Asp	Arg	Lys	Ser	Glu	Phe	Leu	Lys	Thr	Leu	Lys
				320					325				330	
Asp	Asp	Arg	Asn	Gly	Asp	Phe	Ser	Glu	Asn	Arg	Asp	Cys	Asp	Lys
				335					340				345	
Leu	Glu	Asp	Leu	Glu	Asp	Asn	Ser	Thr	Pro	Glu	Pro	Lys	Glu	Asn
				350					355				360	
Gly	Glu	Glu	Gly	Cys	His	Gln	Asn	Gly	Leu	Ala	Leu	Pro	Val	Val
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Glu	Glu	Gly	Glu	Val	Leu	Ser	His	Ser	Leu	Glu	Ala	Glu	His	Arg
				380					385				390	
Leu	Leu	Lys	Ala	Met	Gly	Trp	Gln	Glu	Tyr	Pro	Glu	Asn	Asp	Glu
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Asn	Cys	Leu	Pro	Leu	Thr	Glu	Asp	Glu	Leu	Lys	Glu	Phe	His	Met
				410					415				420	
Lys	Thr	Glu	Gln	Leu	Arg	Arg	Asn	Gly	Phe	Gly	Lys	Asn	Gly	Phe
				425					430				435	
Leu	Gln	Ser	Arg	Ser	Ser	Ser	Leu	Phe	Ser	Pro	Trp	Arg	Ser	Thr
				440					445				450	
Cys	Lys	Ala	Glu	Phe	Glu	Asp	Ser	Asp	Thr	Glu	Thr	Ser	Ser	Ser
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<212> DNA

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<223> unknown base

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cccgatgg cttcatgga gaagccgcca gctggcaagg tgctgctgga 50
cgacacggtg ccgctgacag cagccatcga ggcgagccag agcctgcagt 100
cccacacgga atatattatt cgagtcaaa gaggaatttc tctggaaaac 150
agctggcaga tngtnagaag atacagtgac tttnatntgc ttaacaacag 200
cttnanatt ncaggnctna gnntncctct tcctccnaan aaantgattn 250
ggnaacatgg ancgtgnant tcatngctng anaggcagnn aggt 294

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a 51

<210> 8
<211> 31
<212> DNA
<213> Homo sapiens

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<210> 9
<211> 793
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 379, 433, 459, 492, 517, 541, 549, 561, 575, 579, 582, 710, 742,
774, 784
<223> unknown base

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gacctattgg gacaccttct ggagtatggg aaaacccgcc tagtgccaag 150
caaccctcca agatgctagt tatcaaaaaa gtttccaaag aggatcctgc 200
tgctgcyytc tctgctgcat tcacccatcacc aggtatctcac catgcaaatg 250

ggaacaaatt gtcatccgtg gttccaagtg tctataagaa cctggttct 300
aagcctgtac caccccttc caagccta at gcatggaaag ctaacaggat 350
ggagcacaag tcaggatccc tttcctctna gcccggagtc tgctttacc 400
agtccaatct ctgttaccaa accagtggta ctnggctagt ggtgcagctc 450
tgagttctnc ccaaagagag tccctccagc accacccctc cnaattgaga 500
tcagctcctc tcgtctngac caagttgac ccggcgaacc naccgacang 550
gaagragtga ngttcctgaa aactnctgna anggatgacc gggaatggga 600
agacttlytc agaagaatag agactgtgac aagctggaag atttggagga 650
caacagcaca ctgaacccaa gaaaaatggg ggaggaaggc tgttcatcaa 700
atggtcttn cttcctgta gttggaagga ggggaggttt tntcacattt 750
tttaggagcag agcacaggtt tttnaagttt tggntggcgg att 793

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<211> 24
<212> DNA
<213> Homo sapiens

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<400> 11
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<210> 12
<211> 25
<212> DNA
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<400> 12
cttggtcaga cgagaggagc tgatc 25

<210> 13
<211> 2366
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 103
<223> unknown base

<400> 13
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agtatgtccc ttctctcacc atg agc tgg ctc tcc agt tcc 91

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	1				5								
cag	gga	gtg	gtn	cta	aca	gcc	tac	cac	ccc	agc	ggc	aag	130
Gln	Gly	Val	Xaa	Leu	Thr	Ala	Tyr	His	Pro	Ser	Gly	Lys	
10				15					20				
gac	cag	acc	gtc	ggg	aac	agc	cat	gca	aag	gca	ggg	gag	169
Asp	Gln	Thr	Val	Gly	Asn	Ser	His	Ala	Lys	Ala	Gly	Glu	
25					30								
gaa	gcc	acc	tcg	agt	cgc	aga	tat	ggc	cag	tac	act	atg	208
Glu	Ala	Thr	Ser	Ser	Arg	Arg	Tyr	Gly	Gln	Tyr	Thr	Met	
35					40					45			
aac	cag	gaa	agc	acc	acc	atc	aaa	gtt	atg	gag	aag	cct	247
Asn	Gln	Glu	Ser	Thr	Thr	Ile	Lys	Val	Met	Glu	Lys	Pro	
50						55							
cca	ttt	gat	cga	tca	att	tcc	cag	gat	tct	ttg	gat	gaa	286
Pro	Phe	Asp	Arg	Ser	Ile	Ser	Gln	Asp	Ser	Leu	Asp	Glu	
60					65					70			
cta	tct	atg	gaa	gac	tat	tgg	ata	gaa	cta	gaa	aac	atc	325
Leu	Ser	Met	Glu	Asp	Tyr	Trp	Ile	Glu	Leu	Glu	Asn	Ile	
75					80					85			
aag	aaa	tct	agt	gaa	aac	agc	caa	gaa	gat	caa	gag	gtg	364
Lys	Lys	Ser	Ser	Glu	Asn	Ser	Gln	Glu	Asp	Gln	Glu	Val	
90						95							
gtt	gtt	gtc	aaa	gag	cct	gat	gag	gga	gaa	ttg	gaa	gaa	403
Val	Val	Val	Lys	Glu	Pro	Asp	Glu	Gly	Glu	Leu	Glu	Glu	
100					105					110			
gag	tgg	ctt	aaa	gag	gcc	ggt	tta	tcc	aat	ctc	ttc	gga	442
Glu	Trp	Leu	Lys	Glu	Ala	Gly	Leu	Ser	Asn	Leu	Phe	Gly	
115						120							
gag	tct	gct	gga	gat	cca	cag	gaa	agc	att	gtg	ttt	tta	481
Glu	Ser	Ala	Gly	Asp	Pro	Gln	Glu	Ser	Ile	Val	Phe	Leu	
125					130					135			
tca	aca	ttg	acg	cg	acc	cag	gca	gca	gca	gtt	cag	aag	520
Ser	Thr	Leu	Thr	Arg	Thr	Gln	Ala	Ala	Ala	Val	Gln	Lys	
140					145					150			
cga	gta	gag	acg	gtc	tcc	cag	acc	ttg	agg	aaa	aaa	aac	559
Arg	Val	Glu	Thr	Val	Ser	Gln	Thr	Leu	Arg	Lys	Lys	Asn	
155						160							
aaa	cag	tac	cag	att	cct	gac	gtc	aga	gac	ata	ttt	gct	598
Lys	Gln	Tyr	Gln	Ile	Pro	Asp	Val	Arg	Asp	Ile	Phe	Ala	
165					170					175			
caa	cag	aga	gaa	tca	aaa	gaa	aca	gct	cca	ggt	ggc	act	637
Gln	Gln	Arg	Glu	Ser	Lys	Glu	Thr	Ala	Pro	Gly	Gly	Thr	
180						185							
gaa	tcg	cag	tca	ctt	aga	aca	aat	gaa	aac	aaa	tac	caa	676
Glu	Ser	Gln	Ser	Leu	Arg	Thr	Asn	Glu	Asn	Lys	Tyr	Gln	

190

195

200

gga aga gat gac gag gca tct aac ctt gtt ggt gaa gag 715
 Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu Glu
 205 210 215

aag ctg atc cca cct gag gag acg cct gcc cct gaa aca 754
 Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr
 220 225

gac atc aac ctg gag gta tca ttt gcc gag caa gca ctc 793
 Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu
 230 235 240

aat cag aaa gag aga tcc aag gag aaa atc cag aag agc 832
 Asn Gln Lys Glu Arg Ser Lys Glu Lys Ile Gln Lys Ser
 245 250

aaa ggc gat gat gcc aca tta cct agt ttc aga ttg cca 871
 Lys Gly Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro
 255 260 265

aaa gac aaa acg ggt acc aca agg att ggt gac ctc gca 910
 Lys Asp Lys Thr Gly Thr Arg Ile Gly Asp Leu Ala
 270 275 280

ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att 949
 Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile
 285 290

gag ctg act gcc ctc tat gat gta ttg ggt att gag ctg 988
 Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu
 295 300 305

aaa caa caa aaa gct gtg aaa atc aaa aca aaa gat tct 1027
 Lys Gln Gln Lys Ala Val Lys Ile Lys Thr Lys Asp Ser
 310 315

ggt ctt ttt tgc gtt cca ttg aca gcg cta tta gaa caa 1066
 Gly Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln
 320 325 330

gat cag agg aaa gta cca gga atg cga ata ccc ttg atc 1105
 Asp Gln Arg Lys Val Pro Gly Met Arg Ile Pro Leu Ile
 335 340 345

ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg 1144
 Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu
 350 355

gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att 1183
 Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile
 360 365 370

aga atc aag aat ctt tgc caa gaa cta gaa gca aag ttt 1222
 Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe
 375 380

tat gaa ggg act ttt aat tgg gaa agt gtc aaa cag cat 1261
 Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His
 385 390 395

gat gcc gcc agc ctg ctg aag ctc ttc att cgg gag ttg 1300
 Asp Ala Ala Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu
 400 405 410

ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc ttt 1339
 Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala Phe
 415 420

cag gct gtc cag aat ctt cca acc aag aag cag caa cta 1378
 Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu
 425 430 435

cag gct ttg aac ctt ctt gtc atc ctc cta cct gat gca 1417
 Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp Ala
 440 445

aac agg gac aca ctg aag gcc ctt ctt gaa ttt ctc caa 1456
 Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln
 450 455 460

aga gta ata gat aat aaa gaa aaa aat aaa atg aca gtc 1495
 Arg Val Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val
 465 470 475

atg aat gta gca atg gtc atg gcc ccg aat ctc ttt atg 1534
 Met Asn Val Ala Met Val Met Ala Pro Asn Leu Phe Met
 480 485

tgt cat gca ttg gga ttg aag tcc agt gaa cag cga gaa 1573
 Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu
 490 495 500

ttt gta atg gca gct ggg aca gca aat acc atg cac tta 1612
 Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu
 505 510

ttg att aag tac caa aaa ctt ctg tgg aca att ccc aag 1651
 Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys
 515 520 525

ttt att gta aac caa gtg agg aag caa aac acg gaa aat 1690
 Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn
 530 535 540

cat aaa aag gat aaa aga gcc atg aag aaa ttg ctg aag 1729
 His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys
 545 550

aaa atg gct tat gac cga gaa aaa tat gaa aag caa gat 1768
 Lys Met Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp
 555 560 565

aag agt aca aat gat gct gac gtt cct cag gga gtg att 1807
 Lys Ser Thr Asn Asp Ala Asp Val Pro Gln Gly Val Ile
 570 575

cga gtg caa gct ccc cat ctt tcg aaa gtt tcc atg gca 1846
 Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala
 580 585 590

ata cag cta act gaa gaa cta aaa gcc agt gat gta ctt 1885
Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu
595 600 605

gcc agg ttt ctc agc caa gaa agt ggg gtt gcc cag act 1924
Ala Arg Phe Leu Ser Gln Glu Ser Gly Val Ala Gln Thr
610 615

ctc aag aaa gga gaa gtt ttt ttg tat gaa att gga gga 1963
Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly Gly
620 625 630

aat att ggg gaa cgc tgc ctt gat gat gac act tac atg 2002
Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met
635 640

aag gat tta tat cag ctt aac cca aat gct gag tgg gtt 2041
Lys Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val
645 650 655

ata aag tca aag cca ttg t agaagactta acaagctgca 2080
Ile Lys Ser Lys Pro Leu
660 663

gataaccatg tggacttctg tcataattct tgctgagtca agagtgtaaa 2130
taaaaagaaat ggcaggactc atattattca gttgtaccca agtattttaa 2180
aaatgactct cttaagcctt aaaaagtcat agatttgc tgctgccaga 2230
attatattaa attattatta atggattat tagaaaaaaaaa aatttctgga 2280
gtgagagtaa agaggcttaa ttagttgtg ggcagtttc ttatgctctg 2330
tgaaatgtgt ccagatgtga catagttttt tttttt 2366

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<212> PRT
<213> Homo sapiens

<400> 14
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20 25 30

Ala Gly Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr
35 40 45

Met Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro
50 55 60

Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met
65 70 75

Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu
80 85 90

Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys Glu Pro Asp

95	100	105												
Glu	Gly	Glu	Leu	Glu	Glu	Glu	Trp	Leu	Lys	Glu	Ala	Gly	Leu	Ser
110									115					120
Asn	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Asp	Pro	Gln	Glu	Ser	Ile	Val
125									130					135
Phe	Leu	Ser	Thr	Leu	Thr	Arg	Thr	Gln	Ala	Ala	Ala	Val	Gln	Lys
140									145					150
Arg	Val	Glu	Thr	Val	Ser	Gln	Thr	Leu	Arg	Lys	Lys	Asn	Lys	Gln
155									160					165
Tyr	Gln	Ile	Pro	Asp	Val	Arg	Asp	Ile	Phe	Ala	Gln	Gln	Arg	Glu
170									175					180
Ser	Lys	Glu	Thr	Ala	Pro	Gly	Gly	Thr	Glu	Ser	Gln	Ser	Leu	Arg
185									190					195
Thr	Asn	Glu	Asn	Lys	Tyr	Gln	Gly	Arg	Asp	Asp	Glu	Ala	Ser	Asn
200									205					210
Leu	Val	Gly	Glu	Glu	Lys	Leu	Ile	Pro	Pro	Glu	Glu	Thr	Pro	Ala
215									220					225
Pro	Glu	Thr	Asp	Ile	Asn	Leu	Glu	Val	Ser	Phe	Ala	Glu	Gln	Ala
230									235					240
Leu	Asn	Gln	Lys	Glu	Arg	Ser	Lys	Glu	Lys	Ile	Gln	Lys	Ser	Lys
245									250					255
Gly	Asp	Asp	Ala	Thr	Leu	Pro	Ser	Phe	Arg	Leu	Pro	Lys	Asp	Lys
260									265					270
Thr	Gly	Thr	Thr	Arg	Ile	Gly	Asp	Leu	Ala	Pro	Gln	Asp	Met	Lys
275									280					285
Lys	Val	Cys	His	Leu	Ala	Leu	Ile	Glu	Leu	Thr	Ala	Leu	Tyr	Asp
290									295					300
Val	Leu	Gly	Ile	Glu	Leu	Lys	Gln	Gln	Lys	Ala	Val	Lys	Ile	Lys
305									310					315
Thr	Lys	Asp	Ser	Gly	Leu	Phe	Cys	Val	Pro	Leu	Thr	Ala	Leu	Leu
320									325					330
Glu	Gln	Asp	Gln	Arg	Lys	Val	Pro	Gly	Met	Arg	Ile	Pro	Leu	Ile
335									340					345
Phe	Gln	Lys	Leu	Ile	Ser	Arg	Ile	Glu	Glu	Arg	Gly	Leu	Glu	Thr
350									355					360
Glu	Gly	Leu	Leu	Arg	Ile	Pro	Gly	Ala	Ala	Ile	Arg	Ile	Lys	Asn
365									370					375
Leu	Cys	Gln	Glu	Leu	Glu	Ala	Lys	Phe	Tyr	Glu	Gly	Thr	Phe	Asn
380									385					390
Trp	Glu	Ser	Val	Lys	Gln	His	Asp	Ala	Ala	Ser	Leu	Leu	Lys	Leu
395									400					405

Phe Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu
 410 415 420
 Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln
 425 430 435
 Leu Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp Ala Asn
 440 445 450
 Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile
 455 460 465
 Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn Val Ala Met
 470 475 480
 Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys
 485 490 495
 Ser Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn
 500 505 510
 Thr Met His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile
 515 520 525
 Pro Lys Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn
 530 535 540
 His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met
 545 550 555
 Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn
 560 565 570
 Asp Ala Asp Val Pro Gln Gly Val Ile Arg Val Gln Ala Pro His
 575 580 585
 Leu Ser Lys Val Ser Met Ala Ile Gln Leu Thr Glu Glu Leu Lys
 590 595 600
 Ala Ser Asp Val Leu Ala Arg Phe Leu Ser Gln Glu Ser Gly Val
 605 610 615
 Ala Gln Thr Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly
 620 625 630
 Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met Lys
 635 640 645
 Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val Ile Lys Ser
 650 655 660
 Lys Pro Leu

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 <211> 1327
 <212> DNA
 <213> Homo sapiens

<220>

<221> unsure
<222> 74, 1306
<223> unknown base

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gaccaggcgc cccggcactg cctngtgtga ggggctggca gcttccaac 100
tgcagcaagt ggaggccccct gccagcttcg ggcctgtggg caggggctca 150
gtggggcagg ggtgtggctg ccccgcccg cacgcctgca cctgtctcct 200
ctttgtgacc agtaccgcaa ggggatcatc tcgggctccg tctgccagga 250
cctgtgtgag ctgcat atg gtg gag tgg agg acc tgc ctc 290
Met Val Glu Trp Arg Thr Cys Leu
1 5
tcg gtg gcc ccg ggc cag cag gtg tac agc ggg ctc tgg 329
Ser Val Ala Pro Gly Gln Gln Val Tyr Ser Gly Leu Trp
10 15 20
cg gac aag gat gta acc atc aag tgt ggc att gag gag 368
Arg Asp Lys Asp Val Thr Ile Lys Cys Gly Ile Glu Glu
25 30
acc ctc gac tcc aag gcc cgg tcg gat gcg gcc ccc cgg 407
Thr Leu Asp Ser Lys Ala Arg Ser Asp Ala Ala Pro Arg
35 40 45
cg gag ctg gta ctg ttt gac aag ccc acc cgg ggc acc 446
Arg Glu Leu Val Leu Phe Asp Lys Pro Thr Arg Gly Thr
50 55 60
tcc atc aag gaa ttc cgg gag atg acc ctc ggc ttc ctc 485
Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Gly Phe Leu
65 70
aag gcg aac ctg gga gac ctg cct tcc ctg ccc gctg 524
Lys Ala Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu
75 80 85
gtt ggc cag gtc ctg ctc atg gct gac ttc aac aag gac 563
Val Gly Gln Val Leu Leu Met Ala Asp Phe Asn Lys Asp
90 95
aac cgg gtg tcc ctg ccc gaa gcc aag tcc gtg tgg gcc 602
Asn Arg Val Ser Leu Ala Glu Ala Lys Ser Val Trp Ala
100 105 110
ctg ctg cag cgt aac gag ttc ctg ctg ctg ctg tcc ctg 641
Leu Leu Gln Arg Asn Glu Phe Leu Leu Leu Ser Leu
115 120 125
cag gag aag gag cac gcc tcc aga ctg ctg ggc tac tgt 680
Gln Glu Lys Glu His Ala Ser Arg Leu Leu Gly Tyr Cys
130 135
ggg gac ctc tac ctc acc gag ggc gtg ccg cat ggc gcc 719
Gly Asp Leu Tyr Leu Thr Glu Gly Val Pro His Gly Ala

140

145

150

tgg cac gcg gcc gcc ctc cca ccc ctg ttg cgc cca ctg 758
 Trp His Ala Ala Ala Leu Pro Pro Leu Leu Arg Pro Leu
 155 160

ctg ccg cct gcc ctg cag ggt gct ctc cag cag tgg ctg 797
 Leu Pro Pro Ala Leu Gln Gly Ala Leu Gln Gln Trp Leu
 165 170 175

ggg cct gcg tgg cct tgg cgg gcc aag atc gcc atc ggc 836
 Gly Pro Ala Trp Pro Trp Arg Ala Lys Ile Ala Ile Gly
 180 185 190

ctg ctg gag ttc gtg gag gag ctc ttc cac ggc tct tac 875
 Leu Leu Glu Phe Val Glu Glu Leu Phe His Gly Ser Tyr
 195 200

ggg act ttc tac atg tgt gag acc aca ctg gcc aac gtg 914
 Gly Thr Phe Tyr Met Cys Glu Thr Thr Leu Ala Asn Val
 205 210 215

ggc tac aca gcc acc tac gac ttc aag atg gcc gac ctg 953
 Gly Tyr Thr Ala Thr Tyr Asp Phe Lys Met Ala Asp Leu
 220 225

cag cag gtg gca ccc gag gcc acc gtg cgc cgc ttc ctg 992
 Gln Gln Val Ala Pro Glu Ala Thr Val Arg Arg Phe Leu
 230 235 240

cag ggc cgc cgc tgc gag cac agc acc gac tgc acc tac 1031
 Gln Gly Arg Arg Cys Glu His Ser Thr Asp Cys Thr Tyr
 245 250 255

ggg cgc gac tgc agg gcc ccg tgt gac agg ctc atg agg 1070
 Gly Arg Asp Cys Arg Ala Pro Cys Asp Arg Leu Met Arg
 260 265

cag tgc aag ggc gac ctc atc cag ccc aac ctg gcc aag 1109
 Gln Cys Lys Gly Asp Leu Ile Gln Pro Asn Leu Ala Lys
 270 275 280

gtg tgc gca ctg cta cgg ggc tac ctg ctg cct ggc gcg 1148
 Val Cys Ala Leu Leu Arg Gly Tyr Leu Leu Pro Gly Ala
 285 290

ccc gcc gac ctc cgc gag gag ctg ggc aca cag ctg cgc 1187
 Pro Ala Asp Leu Arg Glu Glu Leu Gly Thr Gln Leu Arg
 295 300 305

acc tgt acc acg ctg agc ggg ctg gcc agc cag gtg gag 1226
 Thr Cys Thr Thr Leu Ser Gly Leu Ala Ser Gln Val Glu
 310 315 320

gcc cat cac tcg ctg gtg ctc agc cac ctc aag act ctg 1265
 Ala His His Ser Leu Val Leu Ser His Leu Lys Thr Leu
 325 330

ctc tgg aag aag atc tcc aac acc aag tac tct t g 1300
 Leu Trp Lys Lys Ile Ser Asn Thr Lys Tyr Ser
 335 340 344

atgggnaatg agggcttgca accttct 1327

<210> 16

<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 104

<223> unknown amino acid

<400> 16

Met Val Glu Trp Arg Thr Cys Leu Ser Val Ala Pro Gly Gln Gln
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Val Tyr Ser Gly Leu Trp Arg Asp Lys Asp Val Thr Ile Lys Cys
20 25 30

Gly Ile Glu Glu Thr Leu Asp Ser Lys Ala Arg Ser Asp Ala Ala
35 40 45

Pro Arg Arg Glu Leu Val Leu Phe Asp Lys Pro Thr Arg Gly Thr
50 55 60

Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Gly Phe Leu Lys Ala
65 70 75

Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu Val Gly Gln Val
80 85 90

Leu Leu Met Ala Asp Phe Asn Lys Asp Asn Arg Val Ser Xaa Ala
95 100 105

Glu Ala Lys Ser Val Trp Ala Leu Leu Gln Arg Asn Glu Phe Leu
110 115 120

Leu Leu Leu Ser Leu Gln Glu Lys Glu His Ala Ser Arg Leu Leu
125 130 135

Gly Tyr Cys Gly Asp Leu Tyr Leu Thr Glu Gly Val Pro His Gly
140 145 150

Ala Trp His Ala Ala Leu Pro Pro Leu Leu Arg Pro Leu Leu
155 160 165

Pro Pro Ala Leu Gln Gly Ala Leu Gln Gln Trp Leu Gly Pro Ala
170 175 180

Trp Pro Trp Arg Ala Lys Ile Ala Ile Gly Leu Leu Glu Phe Val
185 190 195

Glu Glu Leu Phe His Gly Ser Tyr Gly Thr Phe Tyr Met Cys Glu
200 205 210

Thr Thr Leu Ala Asn Val Gly Tyr Thr Ala Thr Tyr Asp Phe Lys
215 220 225

Met Ala Asp Leu Gln Gln Val Ala Pro Glu Ala Thr Val Arg Arg
230 235 240

Phe Leu Gln Gly Arg Arg Cys Glu His Ser Thr Asp Cys Thr Tyr
245 250 255

Gly Arg Asp Cys Arg Ala Pro Cys Asp Arg Leu Met Arg Gln Cys
260 265 270

Lys Gly Asp Leu Ile Gln Pro Asn Leu Ala Lys Val Cys Ala Leu
275 280 285

Leu Arg Gly Tyr Leu Leu Pro Gly Ala Pro Ala Asp Leu Arg Glu
290 295 300

Glu Leu Gly Thr Gln Leu Arg Thr Cys Thr Thr Leu Ser Gly Leu
305 310 315

Ala Ser Gln Val Glu Ala His His Ser Leu Val Leu Ser His Leu
320 325 330

Lys Thr Leu Leu Trp Lys Lys Ile Ser Asn Thr Lys Tyr Ser
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1924, 1939, 1953, 1982, 1991-1992, 2000, 2443

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tgctctngng cnccggcaant cnngggagct actgcaccagg gggcgctacc 150

gggagccctg gcgccgcctg cgaggncgtc gaggcagaacc cagtgacttg 200

attgtaaaaa tttacagagc ggaatcatat gctggctcc aagagttaa 250

agcagcctta gaagatttaa atg cag ttc ttt ttc aac ttc 291

Met Gln Phe Phe Phe Asn Phe

1 5

caa gat tgg cct gaa ggt cta ctt cag gaa ang gaa aaa 330

Gln Asp Trp Pro Glu Gly Leu Leu Gln Glu Xaa Glu Lys

10 15 20

gta ctc tgc gat gct ggt ttt tta ggt gat gcc tta caa 369

Val Leu Cys Asp Ala Gly Phe Leu Gly Asp Ala Leu Gln

25 30

ctc ttt ctt cag tgc tta gcc ctt gat gaa gat ttt gca 408

Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe Ala

35 40 45

cct gca aag ctg caa gta caa aag att tta tgt gat tta 447

Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu
 50 55

tta tta cct gaa aac tta aaa gaa ggc ctg aag gaa tct 486
 Leu Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser
 60 65 70

tcc tgg agt tca tta cca tgt act aaa aac aga cct ttt 525
 Ser Trp Ser Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe
 75 80 85

gat ttt cat tca gtg atg gaa gag tct cag tct ctc aat 564
 Asp Phe His Ser Val Met Glu Glu Ser Gln Ser Leu Asn
 90 95

gaa cct agc cca aag cag agt gaa gaa ata cca gag gtc 603
 Glu Pro Ser Pro Lys Gln Ser Glu Glu Ile Pro Glu Val
 100 105 110

act tca gag cct gtc aaa gga agc tta aac cgt gct cag 642
 Thr Ser Glu Pro Val Lys Gly Ser Leu Asn Arg Ala Gln
 115 120

tca gca cag tct ata aat tca aca gaa atg cct gcc aga 681
 Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro Ala Arg
 125 130 135

gag gac tgt tta aaa aaa gtg tcc tca gaa cct gtt ctg 720
 Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu
 140 145 150

tca gtt caa gaa aaa ggt gtt ctg ctg aaa aga aag ttg 759
 Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu
 155 160

tct ctt tta gaa cag gat gtg att gta aat gaa gat gga 798
 Ser Leu Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly
 165 170 175

aga aat aag ctg aaa aaa caa gga gaa act ccc aat gaa 837
 Arg Asn Lys Leu Lys Gln Gly Glu Thr Pro Asn Glu
 180 185

gtc tgt atg ttt tcc tta gct tat ggt gat att cca gaa 876
 Val Cys Met Phe Ser Leu Ala Tyr Gly Asp Ile Pro Glu
 190 195 200

gaa tta atc gat gtc tca gat ttc gag tgt tct ctc tgc 915
 Glu Leu Ile Asp Val Ser Asp Phe Glu Cys Ser Leu Cys
 205 210 215

atg agg ttg ttt ttt gag cca gta aca acc cct tgc gga 954
 Met Arg Leu Phe Phe Glu Pro Val Thr Thr Pro Cys Gly
 220 225

cat tcg ttc tgt aag aat tgt ctt gag cgt tgt tta gat 993
 His Ser Phe Cys Lys Asn Cys Leu Glu Arg Cys Leu Asp
 230 235 240

cat gca cca tat tgt cct ctt tgc aaa gaa agc tta aat 1032
 His Ala Pro Tyr Cys Pro Leu Cys Lys Glu Ser Leu Asn

245

250

gag tat cta gca gat agg agg tac tgt gtc aca cag ctg 1071
 Glu Tyr Leu Ala Asp Arg Arg Tyr Cys Val Thr Gln Leu
 255 260 265

ttg gaa gaa tta ata gtg aag tat ctg cct gat gaa ctg 1110
 Leu Glu Glu Leu Ile Val Lys Tyr Leu Pro Asp Glu Leu
 270 275 280

tct gag aga aaa aaa ata tat gaa gaa gaa act gct gaa 1149
 Ser Glu Arg Lys Lys Ile Tyr Glu Glu Glu Thr Ala Glu
 285 290

ctc tca cac ttg acc aag aat gtt cca ata ttt gtt tgc 1188
 Leu Ser His Leu Thr Lys Asn Val Pro Ile Phe Val Cys
 295 300 305

act atg gcc tac ccc act gtg cct tgc cct ctc cat gta 1227
 Thr Met Ala Tyr Pro Thr Val Pro Cys Pro Leu His Val
 310 315

ttt gag cca aga tac aga ttg atg att cga aga agt ata 1266
 Phe Glu Pro Arg Tyr Arg Leu Met Ile Arg Arg Ser Ile
 320 325 330

cag act gga acc aaa cag ttt ggc atg tgt gtc agt gat 1305
 Gln Thr Gly Thr Lys Gln Phe Gly Met Cys Val Ser Asp
 335 340 345

aca caa aat agt ttt gca gat tat ggt tgt atg tta caa 1344
 Thr Gln Asn Ser Phe Ala Asp Tyr Gly Cys Met Leu Gln
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att aga aac gtg cat ttc tta ccg gac gga agg tct gtg 1383
 Ile Arg Asn Val His Phe Leu Pro Asp Gly Arg Ser Val
 360 365 370

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 Val Asp Thr Val Gly Gly Lys Arg Phe Arg Val Leu Lys
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 Arg Gly Met Lys Asp Gly Tyr Cys Thr Ala Asp Ile Glu
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 Tyr Leu Glu Asp Val Lys Val Glu Asn Glu Asp Glu Ile
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aag aat ctc aga gag ctt cat gat ttg gtt tac tct caa 1539
 Lys Asn Leu Arg Glu Leu His Asp Leu Val Tyr Ser Gln
 415 420

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 Ala Cys Ser Trp Phe Gln Asn Leu Arg Asp Arg Phe Arg
 425 430 435

agc caa att ctt cag cat ttc gga tca atg ccc gag ang 1617
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Glu Glu Asn Leu Gln Ala Ala Pro Asn Gly Pro Ala Trp
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Cys Trp Trp Leu Leu Ala Val Leu Pro Val Asp Pro Arg
465 470 475

tac cag ctg tcg gtt ttg tca atg aag tct ttg aaa gaa 1734
Tyr Gln Leu Ser Val Leu Ser Met Lys Ser Leu Lys Glu
480 485

cgg ttg acc aag ata cag cat ata ctg acc tat ttt tct 1773
Arg Leu Thr Lys Ile Gln His Ile Leu Thr Tyr Phe Ser
490 495 500

aga gac caa tct aag t a actaactctt tggatctccc 1810
Arg Asp Gln Ser Lys
505 506

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 Ala Leu Gln Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe
 35 40 45

 Ala Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu Leu
 50 55 60

 Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser Ser Trp Ser
 65 70 75

 Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe Asp Phe His Ser Val
 80 85 90

 Met Glu Glu Ser Gln Ser Leu Asn Glu Pro Ser Pro Lys Gln Ser
 95 100 105

 Glu Glu Ile Pro Glu Val Thr Ser Glu Pro Val Lys Gly Ser Leu
 110 115 120

 Asn Arg Ala Gln Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro
 125 130 135

 Ala Arg Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu
 140 145 150

 Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu Ser Leu
 155 160 165

 Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly Arg Asn Lys Leu
 170 175 180

 Lys Lys Gln Gly Glu Thr Pro Asn Glu Val Cys Met Phe Ser Leu
 185 190 195

 Ala Tyr Gly Asp Ile Pro Glu Glu Leu Ile Asp Val Ser Asp Phe

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Glu Cys Ser Leu Cys Met Arg Leu Phe	Phe Glu Pro Val Thr	Thr
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Pro Cys Gly His Ser Phe Cys Lys Asn	Cys Leu Glu Arg Cys	Leu
230	235	240
Asp His Ala Pro Tyr Cys Pro Leu Cys	Lys Glu Ser Leu Asn	Glu
245	250	255
Tyr Leu Ala Asp Arg Arg Tyr Cys Val	Thr Gln Leu Leu Glu	Glu
260	265	270
Leu Ile Val Lys Tyr Leu Pro Asp Glu	Leu Ser Glu Arg Lys	Lys
275	280	285
Ile Tyr Glu Glu Glu Thr Ala Glu Leu	Ser His Leu Thr Lys	Asn
290	295	300
Val Pro Ile Phe Val Cys Thr Met Ala	Tyr Pro Thr Val Pro	Cys
305	310	315
Pro Leu His Val Phe Glu Pro Arg Tyr	Arg Leu Met Ile Arg	Arg
320	325	330
Ser Ile Gln Thr Gly Thr Lys Gln Phe	Gly Met Cys Val Ser	Asp
335	340	345
Thr Gln Asn Ser Phe Ala Asp Tyr Gly	Cys Met Leu Gln Ile	Arg
350	355	360
Asn Val His Phe Leu Pro Asp Gly Arg	Ser Val Val Asp Thr	Val
365	370	375
Gly Gly Lys Arg Phe Arg Val Leu Lys	Arg Gly Met Lys Asp	Gly
380	385	390
Tyr Cys Thr Ala Asp Ile Glu Tyr Leu	Glu Asp Val Lys Val	Glu
395	400	405
Asn Glu Asp Glu Ile Lys Asn Leu Arg	Glu Leu His Asp Leu	Val
410	415	420
Tyr Ser Gln Ala Cys Ser Trp Phe Gln	Asn Leu Arg Asp Arg	Phe
425	430	435
Arg Ser Gln Ile Leu Gln His Phe Gly	Ser Met Pro Xaa Arg	Glu
440	445	450
Glu Asn Leu Gln Ala Ala Pro Asn Gly	Pro Ala Trp Cys Trp	Trp
455	460	465
Leu Leu Ala Val Leu Pro Val Asp Pro	Arg Tyr Gln Leu Ser	Val
470	475	480
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tcagtggttga gtatctcaaa gcctttcagg ctgtccagaa tcttccaacc 200
aagaagcagc aactacaggg ctttgaacc ctttctttta ctcattcctg 250
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tgc 53

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<210> 24

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<213> Homo sapiens

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atataaaacca tggcagca tggtgatcta actgtgatat gaataaggca 200
taactaacat ttgcacccgag accagaatta aaaacaaaaa caaactttaa 250
aagcttagtt ctatattaaa cttcttctt tttcccagat ccttaatggg 300
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aactggtaact gaatttagtt ctccctttac ctttatgtac aattaaatgt 450
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cctggccaaac cagcgccggc agggaaaggca ggtctccag gttcgccctg 150
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<210> 27
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<210> 28
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<400> 28
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<210> 29
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